



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/492,028A

DATE: 09/03/2004

TIME: 11:46:59

Input Set : A:\Uc-926-1.app

Output Set: N:\CRF4\09032004\I492028A.raw

3 <110> APPLICANT: Zuker, Charles S.
 4 The Regents of the University of California
 6 <120> TITLE OF INVENTION: Assays for Sensory Modulators Using a Sensory Cell
 7 Specific G-Protein Alpha Subunit
 9 <130> FILE REFERENCE: 02307E-092610US
 11 <140> CURRENT APPLICATION NUMBER: US 09/492,028A
 12 <141> CURRENT FILING DATE: 2000-01-26
 14 <150> PRIOR APPLICATION NUMBER: US 60/117,367
 15 <151> PRIOR FILING DATE: 1999-01-27
 17 <160> NUMBER OF SEQ ID NOS: 14
 19 <170> SOFTWARE: PatentIn Ver. 2.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1503
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Mus sp.
 26 <220> FEATURE:
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 29 <223> OTHER INFORMATION: mouse taste cell specific G-protein alpha 14
 30 subunit (TC-Galpa14)
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 37 ctccaggtcc ctgtcgctcc gtcgaggtgg caagcc atg gcc ggc tgc tgc tgt 174
 38 Met Ala Gly Cys Cys Cys
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 41 ttg tct gcg gag gag aaa gag tct cag cgc atc agc gcg gag atc gag 222
 42 Leu Ser Ala Glu Glu Lys Glu Ser Gln Arg Ile Ser Ala Glu Ile Glu
 43 10 15 20
 45 cgg cac gtt cgc cgc gac aag aag gac gcg cgc cgg gag ctc aag ctg 270
 46 Arg His Val Arg Arg Asp Lys Lys Asp Ala Arg Arg Glu Leu Lys Leu
 47 25 30 35
 49 ctg ttg ctg gga acc ggt gag agt ggg aaa agc acc ttt atc aag cag 318
 50 Leu Leu Leu Gly Thr Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln
 51 40 45 50
 53 atg agg ata atc cat ggg tct ggc tac agt gat gaa gat aga aag ggc 366
 54 Met Arg Ile Ile His Gly Ser Gly Tyr Ser Asp Glu Asp Arg Lys Gly
 55 55 60 65 70
 57 ttc acg aag ctg gtt tac caa aac ata ttc acg gcc atg caa gcc atg 414
 58 Phe Thr Lys Leu Val Tyr Gln Asn Ile Phe Thr Ala Met Gln Ala Met
 59 75 80 85
 61 atc aga gca atg gat acc ctg agg ata caa tac atg tgt gag cag aat 462
 62 Ile Arg Ala Met Asp Thr Leu Arg Ile Gln Tyr Met Cys Glu Gln Asn



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66 Lys Glu Asn Ala Gln Ile Ile Arg Glu Val Glu Val Asp Lys Val Thr				
67	105	110	115	
69 gca ctc tct aga gac cag gtg gca gcc atc aag cag ctg tgg ctg gat				558
70 Ala Leu Ser Arg Asp Gln Val Ala Ala Ile Lys Gln Leu Trp Leu Asp				
71	120	125	130	
73 ccc gga atc cag gag tgt tac gac agg agg agg gag tac cag ctg tca				606
74 Pro Gly Ile Gln Glu Cys Tyr Asp Arg Arg Arg Glu Tyr Gln Leu Ser				
75 135	140	145	150	
77 gac tct gcc aaa tat tac ctg acg gac att gag cgt atc gcc atg ccc				654
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81 tct ttc gtg cca aca caa cag gat gtg ctt cgt gtt aga gtg ccc acc				702
82 Ser Phe Val Pro Thr Gln Gln Asp Val Leu Arg Val Arg Val Pro Thr				
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85 act ggc atc ata gaa tat cca ttc gac ctg gaa aac atc atc ttc cga				750
86 Thr Gly Ile Ile Glu Tyr Pro Phe Asp Leu Glu Asn Ile Ile Phe Arg				
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89 atg gtg gat gtt ggt ggc cag cga tct gaa cga cgg aaa tgg att cac				798
90 Met Val Asp Val Gly Gly Gln Arg Ser Glu Arg Arg Lys Trp Ile His				
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94 Cys Phe Glu Ser Val Thr Ser Ile Ile Phe Leu Val Ala Leu Ser Glu				
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97 tat gac cag gtt ctg gct gag tgt gac aat gag aac cgc atg gag gag				894
98 Tyr Asp Gln Val Leu Ala Glu Cys Asp Asn Glu Asn Arg Met Glu Glu				
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121 gct aca gac acc gag aat atc cgc ttt gtg ttt gct gct gtc aaa gac				1182
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125 aca atc cta cag cta aac cta cgg gag ttc aac ttg gtg taa				1224
126 Thr Ile Leu Gln Leu Asn Leu Arg Glu Phe Asn Leu Val				
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157 35 40 45
159 Ser Thr Phe Ile Lys Gln Met Arg Ile Ile His Gly Ser Gly Tyr Ser
160 50 55 60
162 Asp Glu Asp Arg Lys Gly Phe Thr Lys Leu Val Tyr Gln Asn Ile Phe
163 65 70 75 80
165 Thr Ala Met Gln Ala Met Ile Arg Ala Met Asp Thr Leu Arg Ile Gln
166 85 90 95
168 Tyr Met Cys Glu Gln Asn Lys Glu Asn Ala Gln Ile Ile Arg Glu Val
169 100 105 110
171 Glu Val Asp Lys Val Thr Ala Leu Ser Arg Asp Gln Val Ala Ala Ile
172 115 120 125
174 Lys Gln Leu Trp Leu Asp Pro Gly Ile Gln Glu Cys Tyr Asp Arg Arg
175 130 135 140
177 Arg Glu Tyr Gln Leu Ser Asp Ser Ala Lys Tyr Tyr Leu Thr Asp Ile
178 145 150 155 160
180 Glu Arg Ile Ala Met Pro Ser Phe Val Pro Thr Gln Gln Asp Val Leu
181 165 170 175
183 Arg Val Arg Val Pro Thr Thr Gly Ile Ile Glu Tyr Pro Phe Asp Leu
184 180 185 190
186 Glu Asn Ile Ile Phe Arg Met Val Asp Val Gly Gly Gln Arg Ser Glu
187 195 200 205
189 Arg Arg Lys Trp Ile His Cys Phe Glu Ser Val Thr Ser Ile Ile Phe
190 210 215 220
192 Leu Val Ala Leu Ser Glu Tyr Asp Gln Val Leu Ala Glu Cys Asp Asn
193 225 230 235 240
195 Glu Asn Arg Met Glu Glu Ser Lys Ala Leu Phe Arg Thr Ile Ile Thr
196 245 250 255
198 Tyr Pro Trp Phe Leu Asn Ser Ser Val Ile Leu Phe Leu Asn Lys Lys
199 260 265 270
201 Asp Leu Leu Glu Glu Lys Ile Met Tyr Ser His Leu Ile Ser Tyr Phe
202 275 280 285

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210 Tyr Ser His Phe Thr Cys Ala Thr Asp Thr Glu Asn Ile Arg Phe Val
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